REMARKS

Claims 1-77 are pending and subject to restriction.

Claims 2-16, 18, 25-38, 46-56, 60, 63-66, and 68-76 have been withdrawn herein without prejudice.

Group election:

The Examiner is requesting an initial election of one Group of claims from among:

Groups I (claims 1-24, 39, and 45-77);

Group II (claims 25-38 and 40-44); and

Group III (claim 39 in part).

Additional election:

With respect to Group I, the Examiner is additionally requesting restriction to one or a particular combination of gene species from the following:

STMN1, SFN, S100A2, TGRBR2, TP53, PTGS2, FGFR1, SYK, PITX2, GRIN2D, PSA, CGA, CYP2D6, MSMB, COX7A2L, VTN, PRKCD, ONECUT2, WBP11, CYP2D~DAG1, ERBB2, S100A2, TFF1, TP53, TMEFF2, ESR1, SYK, RASSF1, PITX2, PSAT1, CGA, and PCAF.

Further election:

With respect to Group I, the Examiner is further requesting restriction to one or a particular combination of target nucleic acid sequence species recited in claims 15-19, 39 and 45-77.

Yet further election:

Additionally, with respect to Group I, the Examiner is yet further requesting restriction to one or a particular combination of the oligonucleotides recited in claims 50-54, 55-56 (i.e., the oligonucleotides of claims 3-35), and 59-60.

Election

Applicants elect **Group I** (claims 1-24, 39, and 45-77), additionally elect PITX2, further elect SEQ ID NO:83. ***with traverse***. Claims which required a restriction to a particular oligo have

been withdrawn herein without prejudice.

Applicants' traversal:

The basis of Applicants' traversal is two fold.

First. As disclosed at pages 29 and 50 of the specification, SEQ ID NO:83 and SEQ ID NO:135 are particularly preferred regions of PITX2 (*i.e.*, PITX2 comprises both SEQ ID NO:83 and SEQ ID NO:135), and in preferred embodiments, the methylation status of CpG positions within SEQ ID NO:83 and SEQ ID NO:135 are determined. Therefore, Applicants contend that these should be grouped together because they correspond to the same gene PITX2 gene sequence, such that a search with respect to PITX2 would easily cover SEQ ID NOS:83 and 135, and little if any additional search burden is represented by inclusion of SEQ ID NOS:83 and 135.

Second. As disclosed at page 50, in particular aspects, the genomic DNA sample is treated in such a manner that cytosine bases which are unmethylated at the 5'-position are converted to uracil, thymine, or another base which is dissimilar to cytosine in terms of hybridization behavior. It is preferred that this treatment is carried out with bisulfite (hydrogen sulfite, disulfite) and subsequent alkaline hydrolysis.

Therefore, SEQ ID NOS:411, 412, 685, and 686 should be grouped and examined together with SEQ ID NO:83 because they correspond to bisulfite-treated sequences for the identical sequence region of genomic SEQ ID NO:83. Specifically, SEQ ID NOS:411and 685 are chemically treated sequences of the sense strand of SEQ ID NO:83 and SEQ ID NOS:412 and 686 are chemically treated sequences of the *complementary* antisense strand of SEQ ID NO:83 (that is, of the identical sequence region of genomic DNA), and the patentability of claims limited by these SEQ ID NOS will be determined based, *inter alia*, on the novelty of analysis based on this genomic sequence region for the claimed indications.

Likewise, SEQ ID NOS:515, 516, 789, and 790 should be grouped and examined together with SEQ ID NO:135 because they correspond to bisulfite-treated sequences for the identical sequence region of genomic SEQ ID NO:135. Specifically, SEQ ID NOS:515 and 789 are chemically treated sequences of the sense strand of SEQ ID NO:135 and SEQ ID NOS:516 and

790 are chemically treated sequences of the *complementary* antisense strand of SEQ ID NO:135 (that is, of the identical sequence region of genomic DNA).

In summary, Applicants point out that it has been the consistent practice of the Office to group the bisulfite-treated sequences with the underlying genomic sequence in a single group, and further point out that SEQ ID NOS:83 and 135 are encompassed within PITX2.

Applicants, therefore, respectfully submit that the elected group should be Group I, PITX2, and in some aspects limited to SEQ ID NOS:83, 135, 411, 412, 685, 686, 515, 516, 789, and 790. This is because the patentability of the claims limited by these SEQ ID NOS will be determined based, *inter alia*, on the novelty of analysis based on this genomic sequence region corresponding to PITX2 that encompasses both SEQ ID NOS:83 and 135.

At a very minimum, Applicants submit that the elected group should be **Group I**, PITX2, SEQ ID NOS:83, 135, 411, 412, 685 and 686, but contend that Group I, PITX2, SEQ ID NOS:83, 135, 411, 412, 685, 686, 515, 516, 789, and 790 would not represent undue burden.

Claim Amendments

Minor amendments to the claims have been made to clarify the claimed subject matter, the amendments all being supported by the originally filed specification including the claims thereof.

No new matter has been added.

Conclusion

Applicants respectfully request entry of the present Response and Amendment, and submit that the elected group should be Group I, PITX2, SEQ ID NOS:83, 135, 411, 412, 685, 686, 515, 516, 789, and 790.

Respectfully submitted,
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